

SEQUENCE LISTING

<110> Zoon, et al.
<120> Interferon Alpha Hybrids
<130> 4239-56957
<140> US 09/744,754
<141> 2001-01-24
<150> US 60/094,407
<151> 1998-07-28
<150> PCT/US99/15284
<151> 1999-07-06
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

gaa gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

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Ser Leu Arg Ser Lys Glu
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc 288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gaa gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
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Ser Leu Arg Ser Lys Glu
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
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ctc ctg gca cag atg agg aga atc tct ctt ttc tcc tgc ttg aag gac 96
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

aga cgt gac ttt gga ttt ccc cag gag gag ttt ggc aac cag ttc caa 144
Arg Arg Asp Phe Gly Phe Pro Gln Glu Phe Gly Asn Gln Phe Gln
35 40 45

aag gct gaa acc atc cct gtc ctc cat gag atg atc cag cag atc ttc 192
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc ctc 240
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc gag 288
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg aat 336
Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn
100 105 110

gtg gac tcc atc ctg gct gtg aag aaa tac ttccaa aga atc act ctt 384
Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

tat ctg aca gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc aga 432
Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa aga 480
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu Arg
145 150 155 160

tta agg agg aag gaa tg 497
Leu Arg Arg Lys Glu
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Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
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Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn
100 105 110

Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

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145 150 155 160

Leu Arg Arg Lys Glu
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<400> 15
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aagttcagtg taaaattttt c

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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc 288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttccaa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

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Ser Leu Arg Ser Lys Glu

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<400> 30

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

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145 150 155 160

Ser Leu Arg Ser Lys Glu
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc 288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttccaa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

agt tta aga agt aag gaa tg 500
Ser Leu Arg Ser Lys Glu

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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

aat gtg gac tcc atc ttg gct gtg aag aaa tac ttc caa aga atc act 384
Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctt tat ctg aca gag aag aaa tac agc cct tgt gct tgg gag gtt gtc 432
Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
145 150 155 160

aga tta agg agg aag gaa tg 500
Arg Leu Arg Arg Lys Glu

<210> 34
<211> 166
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20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

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145 150 155 160

Arg Leu Arg Arg Lys Glu
165

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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288
Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

agt tta aga agt aag gaa tg 500
Ser Leu Arg Ser Lys Glu

<210> 36
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 37
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene Fusion

<220>
<221> CDS
<222> (1)..(498)
<223>

<400> 37
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc 288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

agt tta aga agt aag gaa tg 500
Ser Leu Arg Ser Lys Glu

<210> 38
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 39
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene Fusion

<220>
<221> CDS
<222> (1)..(498)
<223>

<400> 39
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc 288
Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
Leu Tyr Leu Lys Glu Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

agt tta aga agt aag gaa tg 500
Ser Leu Arg Ser Lys Glu

<210> 40
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

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<210> 41
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Gene Fusion

<220>
<221> CDS
<222> (1)..(498)
<223>

<400> 41
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata      48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1           5           10          15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac      96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20          25          30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc      144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35          40          45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc      192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50          55          60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc      240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65          70          75          80

ctc cta gac aaa ttc tac act gaa ctc aac cag cag ctg aat gac ctc      288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85          90          95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg      336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100         105         110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act      384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115         120         125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc      432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130         135         140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa      480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145         150         155         160

agt tta aga agt aag gaa tg                                         500
Ser Leu Arg Ser Lys Glu

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<210> 42
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165